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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

PATENT

P03815US1

ISURF 2413

APPLICANT: Rothschild, et al. GROUP ART NO: 1655
SERIAL NO: 09/380,419 EXAMINER: Goldberg, J.
FILED: July 24, 2000
TITLE: MELANOCORTIN4 RECEPTOR GENE AND USE AS A
GENETIC MARKER FOR FAT CONTENT, WEIGHT GAIN,
AND/OR FEED CONSUMPTION OF ANIMALS

TRANSMITTAL LETTER

To the Commissioner of Patents and Trademarks
Washington, D.C. 20231

Dear Sir:

In response to the Notice to Comply with Sequence Rules
dated January 30, 2001, enclosed please find the following
documents:

1. A copy of the Notice to Comply with
Requirements for Patent Applications Containing
Nucleotide Sequence and/or Amino Acid Sequence
Disclosures (7 pages);
2. Computer readable copy of the "Sequence
Listing";
3. Paper copy of "Sequence Listing" (9 pages);
4. Statement that the Content of the paper and
computer readable copies are the same and
include no new matter (2 pages).

=====

CERTIFICATE OF MAILING (37 C.F.R. § 1.8(a))

I hereby certify that this Transmittal Letter is being deposited with
the United States Postal Service on the date shown below with sufficient
postage as first class mail in an envelope addressed to the Assistant
Commissioner for Patents, Washington, D.C. 20231, this 23rd day of
February, 2001.


Heidi S. Nebel

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No fees are believed to be due at this time, however if
any additional fees are needed, please charge Deposit
Account No. 26-0084.

Respectfully submitted,

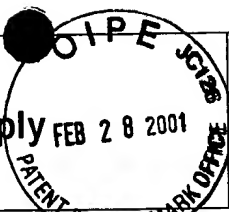


Heidi S. Nebel, Reg. No. 37,719
ZARLEY, MCKEE, THOMTE, VOORHEES
& SEASE

801 Grand - Suite 3200
Des Moines, Iowa 50309-2721
telephone 515-288-3667
facsimile 515-288-1338

CUSTOMER NO. 22885
ATTORNEYS OF RECORD

-pw-

Notice to Comply

Application No.

09/380,419

Examiner

Jeanine Enewold Goldberg

Applicant(s)

ROTHSCHILD ET AL.

Art Unit

1655

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

**RAW SEQUENCE LISTING
ERROR REPORT**

BIOTECH
SYSTEMS
BRANCH

E



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer-readable form:

Application Serial Number:

09/380,419

Source:

1655

Date Processed by STIC:

12/20/2000

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

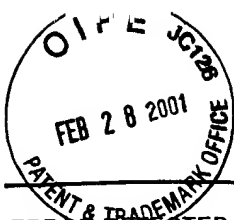
Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/380,419

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/380,419

DATE: 12/29/2000
TIME: 15:02:54

Input Set : A:\MC4R.txt
Output Set : N:\CRF3\12202000\I380419.raw

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Rothschild, Max P.
2 Kim, Kwan Suk
3 Emmett, Rebecca S.
4
5 <120> TITLE OF INVENTION: Melanocortin-4 Receptor Gene and Use as a Genetic
6 Marker for Fat Content, Weight Gain, and/or Feed
7 Consumption in Animals
8
9
10 <130> FILE REFERENCE: rothschild mc4r2
11
12 <140> CURRENT APPLICATION NUMBER: 09/380,419
13
14 <141> CURRENT FILING DATE: 2000-07-24
15
16 <150> PRIOR APPLICATION NUMBER: PCT/US99/16862
17
18 <151> PRIOR FILING DATE: 1999-07-26
19
20 <160> NUMBER OF SEQ ID NOS: 26
21
22 <170> SOFTWARE: PatentIn Ver. 2.0

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ERRORED SEQUENCES

23 <210> SEQ ID NO: 1
24 <211> LENGTH: 745
25 <212> TYPE: DNA
26 <213> ORGANISM: porcine
27 <220> FEATURE:
28
29 <221> NAME/KEY: Variation
30 <222> LOCATION: (678)
31 <223> OTHER INFORMATION: G/A
32 <400> SEQUENCE: 1
33
34 acaagaatct qcatcaccr atgtactttt tcatctatag ctgagctgtg gctqatatgc 60
35 tggtagagct tlecaatggg tgaagaacca ttgtcaccac cctattaaac agcaggaca 120
36 cggagcgaca gaggttcaaa ggaatattt ataatgtat tgcctcagtg atctgttagct 180
37 cctactctgc ctcaatttgc agcctgcttt cgtttcaggt ggcacagtat tttactatct 240
38 ttatgtctct ccagtaccat accattatga cagttlaagcy ggttggatc atcatcagtt 300
39 ghatctgggc agtctgcacg gtgtcgggtg tttgtttcat cacttactca gatagcagtg 360
40 ctgtttattat ctgcctcata adcggtttct taccctagct ggtctctatg gcttctctct 420
41 atgtccacat gtctccatg accagactcc acattaaag gctcgcctc ctcccaagca 480
42 ctggcaccat ccgccaggt ggcacatga agggggcaat taccctgacc atcttgattg 540
43 ggtctcttct ggtctctctg gccctctct tctccactt aatattctat atctcctgca 600
44 ccagaatcc atactgttg tgcctctat ctcactttaa ttgtatctc atctgtatca 660
45 tgtglaattc catcactat cccctgattt atgcactccg gagccaagaa ctgaggaaaa 720
E--> 46 ccttcaaga gatcatctgt tgctat 746

746 shown

Per Sequence Rules, use "r" to represent
g or a; "g" can
only represent
itself

see next pages for more errors

09/380,419 2

<210> 3
<211> 311
<212> PRT
<213> Homo sapiens

see p. 3

<400> 3
Gln Leu Phe Val Ser Pro Glu Val Phe Val Thr Leu Gly Val Ile Ser
1 5 10 15
Leu Leu Glu Asn Ile Leu Val Ile Val Ala Ile Ala Lys Asn Lys Asn
20 25 30
Leu His Ser Pro Met Tyr Phe Phe Ile Cys Ser Leu Ala Val Ala Asp
35 40 45
Met Leu Val Ser Val Ser Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu
50 55 60
Leu Asn Ser Thr Asp Thr Asp Ala Gln Ser Phe Thr Val Asn Ile Asp
65 70 75 80
Asn Val Ile Asp Ser Val Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys
85 90 95
Ser Leu Leu Ser Ile Ala Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala
100 105 110
Leu Gln Tyr His Asn Ile Met Thr Val Lys Arg Val Gly Ile Ser Ile
115 120 125
Ser Cys Ile Trp Ala Ala Cys Thr Val Ser Gly Ile Leu Phe Ile Ile
130 135 140
Tyr Ser Asp Ser Ser Ala Val Ile Ile Cys Leu Ile Thr Met Phe Phe
145 150 155 160
Thr Met Leu Ala Leu Met Ala Ser Leu Tyr Val His Met Phe Leu Met
165 170 175
Ala Arg Leu His Ile Lys Arg Ile Ala Val Leu Pro Gly Thr Gly Ala
180 185 190
Ile Arg Gln Gly Ala Asn Met Lys Gly Ala Ile Thr Leu Thr Ile Leu
195 200 205
Ile Gly Val Phe Val Val Cys Trp Ala Pro Phe Phe Leu His Leu Ile
210 215 220
Phe Tyr Ile Ser Cys Pro Gln Asn Pro Tyr Cys Val Cys Phe Met Ser
225 230 235 240
His Phe Asn Leu Tyr Leu Ile Leu Ile Met Cys Asn Ser Ile Ile Asp
245 250 255
Pro Leu Ile Tyr Ala Leu Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys
260 265 270

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09/380,419 3

Glu Ile Ile Cys Cys Tyr Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser
275 280 285

Arg Tyr Ala Pro Pro Glu Asn Asp Ile Xaa Val Ile Cys Asn Phe Ile
290 295 300

Asp Glu Asn Thr Ile Ala Leu
305 310

See item 10 on Enol
Summary sheet

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/380,419

DATE: 12/20/2006
TIME: 15:02:55

Input Set : A:\MC4R.txt
Output Set: N:\CRF3\12202000\I380419.raw

L:46 M:252 E: No. of Seq. differs. <211>LENGTH:Input:745 Found:745 SEQ:1
L:129 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#13
L:129 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#13
L:129 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#13
L:129 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#13
L:129 M:340 W: (46) "n" or "Naa" used: Feature required, for SEQ ID#13